

FIG. 1

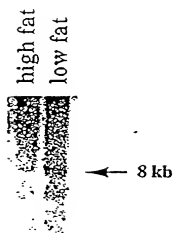


FIG. 2

mouse Bcl-2 →

αActin →

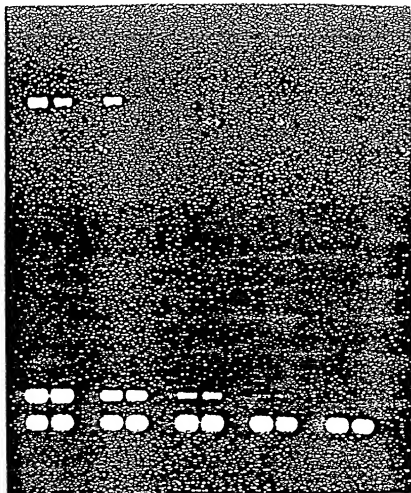


FIG. 3

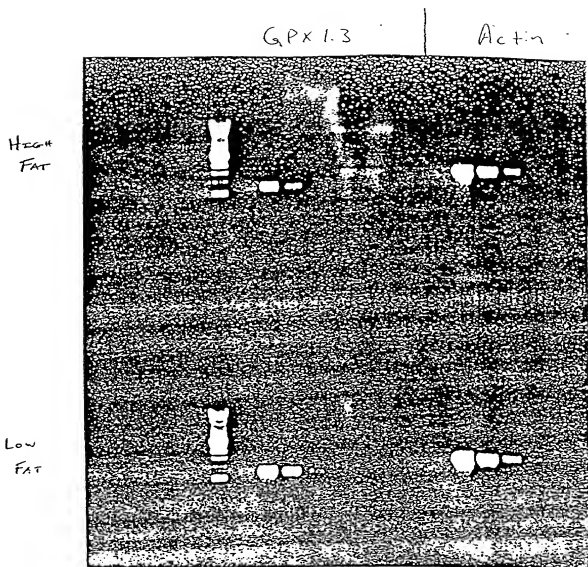


FIG. 4

09970820-100501
105007-02802660

09970820.100501

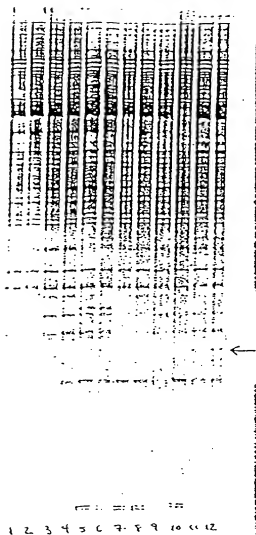


FIG. 5

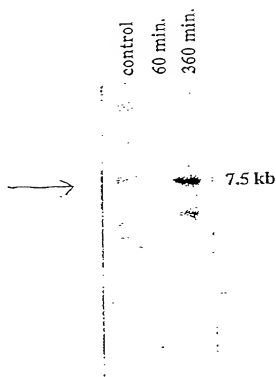


FIG. 6

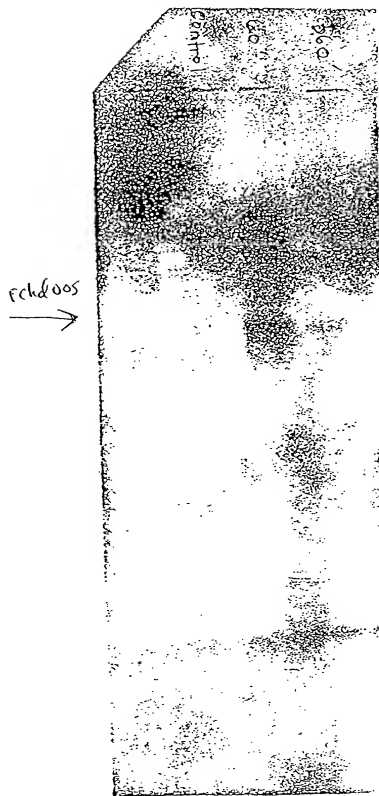


FIG. 7

09970820-106501

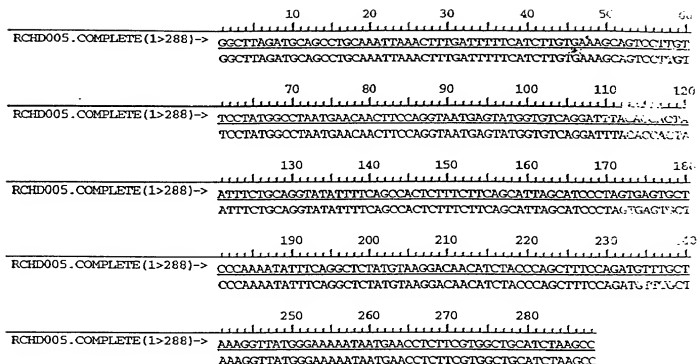


FIG. 8

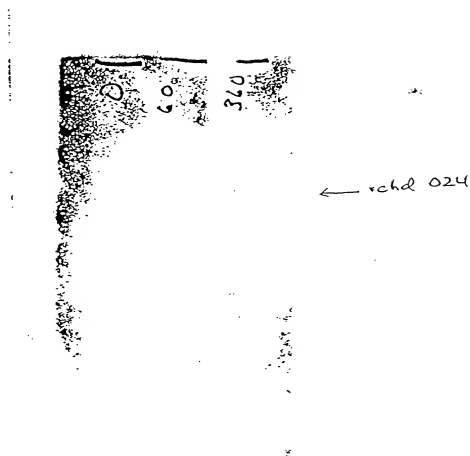
09970320-100501



rchd
024

FIG. 9

123456



2

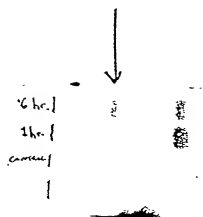


FIG. 11

09370820-100504

10 20 30 40 50
 RCHD024.COMPLETE.SEQ(1>178)-> AAAAATAAATAAATTAAAGTCTGAGACCAATTGGCCAGTGTGAATATAAG
AAAAATAAATAAATTAAAGTCTGAGACCAATTGGCCAGTGTGAATATAAG

60 70 80 90 100
 RCHD024.COMPLETE.SEQ(1>178)-> CACATTACCCCGAGGAGGCCAAGAACTACACAAACCTCTCTATGAGAA
CACATTACCCCGAGGAGGCCAAGAACTACACAAACCTCTCTATGAGAA

110 120 130 140 150
 RCHD024.COMPLETE.SEQ(1>178)-> TTTACCAGTCTCTCTTTCATTGGCAAGAAAAAGCTCAGGAAAATTGCTT
TTTACCAGTCTCTCTTTCATTGGCAAGAAAAAGCTCAGGAAAATTGCTT

160 170
 RCHD024.COMPLETE.SEQ(1>178)-> GTTTAAATTCATGAGCCTAGTCTATGG
GTTTAAATTCATGAGCCTAGTCTATGG

FIG. 12

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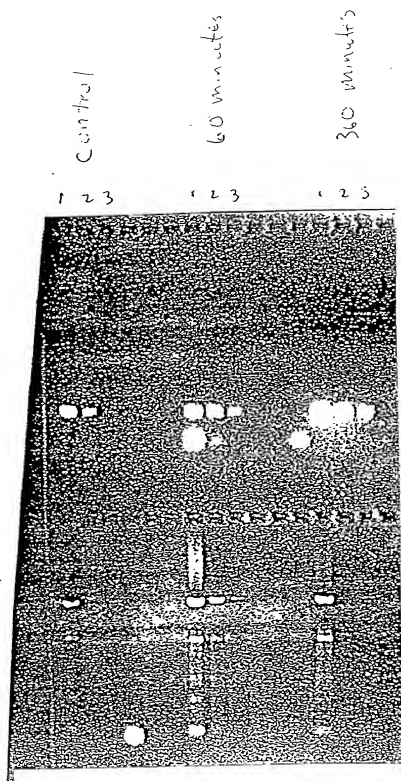


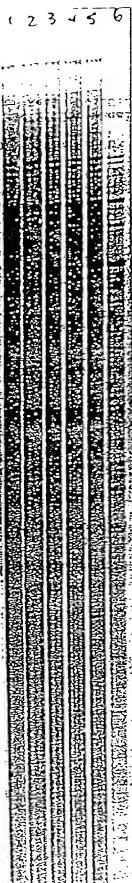
FIG. 14

10 20 30 40 50
 RCHD032 . COMPLETE . SEQ (1>101)-> GGGTAATTCATTAATTACACTTTAAAAATGGAAAGTGGGATAAGAAATCT
 GGGTAATTCATTAATTACACTTTAAAAATGGAAAGTGGGATAAGAAATCT

60 70 80 90 100
 RCHD032 . COMPLETE . SEQ (1>101)-> AAAGTAAACGAGCTTATCTTTTGAAACAATATTATTTTGAATTTGGCTTTA
 AAAGTAAACGAGCTTATCTTTTGAAACAATATTATTTTGAATTTGGCTTTA

RCHD032 . COMPLETE . SEQ (1>101)-> A
 A

FIG. 15



← rchd 036

FIG. 16

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↑ rch 036

FIG. 17

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09970820.100501

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                                10      20      30      40      50
RCHD036.COMPLETE.SEQ(1>184)-> GGCTTGGTGGTGATGCCTACAAGAAATGTTTACATACAAACACTCTATAC
                                60      70      80      90     100
                                GGCTTGGTGGTGATGCCTACAAGAAATGTTTACATACAAACACTCTATAC

                                60      70      80      90     100
RCHD036.COMPLETE.SEQ(1>184)-> ATCTAACTCCGAAAAAGGACCAGCTATTTGGGCAACAGAAAAAGACAA
                                110     120     130     140     150
                                ATCTAACTCCGAAAAAGGACCAGCTATTTGGGCAACAGAAAAAGACAA

                                110     120     130     140     150
RCHD036.COMPLETE.SEQ(1>184)-> GCATTTTCAGAGGAGCGTTGCTTTTCCCTTAAAGACCTAACTCACTTAAGTCT
                                160     170     180
                                GCATTTTCAGAGGAGCGTTGCTTTTCCCTTAAAGACCTAACTCACTTAAGTCT

                                160     170     180
RCHD036.COMPLETE.SEQ(1>184)-> TACAAACAGAAATAACAAGGAGGACAATTTTCTA
                                TACAAACAGAAATAACAAGGAGGACAATTTTCTA

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FIG. 18

0970820-10501

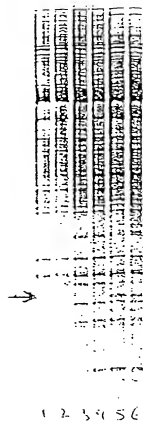


FIG. 19

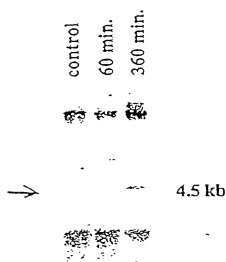


FIG. 20

1 2 3
— — —
[Illegible text]

[Illegible text] ←

[Illegible text]

FIG. 21

09970820-100501

10 20 30 40 50 60
 RCHD502K.COMPLET(1>284)-> CTTGGGATGCTGTTTGGAGGAATCCTCATGAAGGCGCTTGTGTTTCTCTACAAAGCCAT
 CTTGGGATGCTGTTTGGAGGAATCCTCATGAAGGCGCTTGTGTTTCTCTACAAAGCCAT

70 80 90 100 110 120
 RCHD502K.COMPLET(1>284)-> TCCCCCATAGCTACCAACCATCATCAACATCTCCATGATCCTTTGAGTTCCTTTGTTCCT
 TCCCCCATAGCTACCAACCATCATCAACATCTCCATGATCCTTTGAGTTCCTTTGTTCCT

130 140 150 160 170 180
 RCHD502K.COMPLET(1>284)-> CATGGGATGCTCCACCCCACTGTGGCGGAAGTCTACCCCCCTAGCACATCAAGTTCCTAT
 CATGGGATGCTCCACCCCACTGTGGCGGAAGTCTACCCCCCTAGCACATCAAGTTCCTAT

190 200 210 220 230
 RCHD502K.COMPLET(1>284)-> ACATCGGAGTCTCTGCTGCTGCGGAGGACTGCTGCTGCGGAGATTCATCTTCCACCC
 ACATCGGAGTCTCTGCTGCTGCGGAGGACTGCTGCTGCGGAGATTCATCTTCCACCC

250 260 270 280
 RCHD502K.COMPLET(1>284)-> GCTCTGTGGAGACAATGGAATCGAGTACCTCTCCCTTGCCATG
 GCTCTGTGGAGACAATGGAATCGAGTACCTCTCCCTTGCCATG

FIG. 22

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rchd505 →



1 2 3 4 5 6

FIG. 23

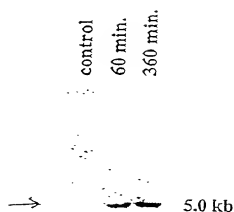


FIG. 24



FIG. 25

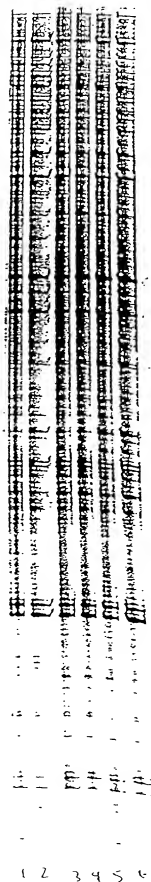


FIG. 26

105001-0280660

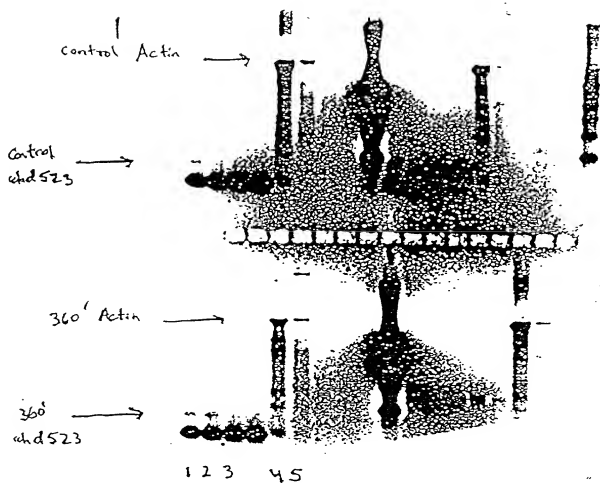


FIG. 27

[illegible]

1

S N S C L N P L I Y S F L G E T F R D K 334
 TTC AAC AGC TGC CTA AAC CCC CTC ATC TAC AGC TTT CTC GGG GAG AOC TTC AGG GAC AAG 1560
 L R L Y I E Q K T N L P A L D R F C H A 354
 CTG AGG CTG TAC ATT GAG CAG AAA ACA AAT TTG CCG GGC CTG GAC GGC TTC TGT CAC GCT 1620
 A L K A V I P D S T E Q S D V R F S S A 374
 GGC CTG AAG GGC GTC ATT CCA GAC AGC AOC GAG CAG TGG GAT GTG AGG TTC AGC AGT GGC 1680
 V * 375
 GTG TAG ACAGGCTTGGCCCATAGGCCAGCCAGGTTGTGACTGGGGAGTCACACAGCTGGTGGACAGAGGCA 1757
 CGGCGAGTCACTGTCTAAACTGGGTGAGTGTGGCTTCTGCTCTCTGGGCTCTGGAGGGTCAAGCTTGGCTGGT 1836
 CAGCTGGGGCTGCTTAGGAAAGCTCAGGACTGGTCACTTGCATCTCCACACAGAAATGCTACAAATGCCAAGGGCT 1915
 CGCCCGGAGGGTCCAAAGGCCAGGGTGACCGAGCTGTCAACCGAGCTCTCCCGCGCAAGCTGCTGCGGCTGCGAC 1994
 TGCCCGCTCTGCGAGGAACATTTCTGACACCGTGGACCGAGGAAGCCACAGGGAGGGCACTGTGGGTGAAGCGCT 2073
 CAGTACACAGGAGGCTTAAGCAAACTGCCACCGTGGGGAACTGAGCTGGAGTCCAGGTGCTGGTGGGTCTGA 2152
 GCTGGAGTTCGGGTGTGTCTCTGTGGCCACGGTCTGAGCTAGGCTAGCGCACCGCGAGTTAAAGAGGAGAGGAAAA 2231
 CATGTGCTCTGGTGCAGGCTGAGGCTCTCCATCTTCAGGATGGCAGCAATGGCTGTGGGGCTCACCGAGGCC 2310
 AAGAGAGCGACAGGCTTCGGCCGGAGCAGCAGAGGCGCCCTCTGTGGAGGCGCCCGGCTGTGCTCGGGGTGTCTG 2389
 AGTCACTGCTTGTGACATCAACATGGCAATTGCATCATGTGACTGGGACCGTGGAGCTGGCGGTGGGTGATGTG 2468
 GGTGGCAGGACATGAATATCTCCAGCACTGTGGCTGACGAATTCGTTCTACAGAAATACAGCTGGGGACAACTGC 2547
 GATGATGATGAATAAAGCTTCCCATAAATAGGC 2582

FIG. 28B



FIG. 29

09970820 130501

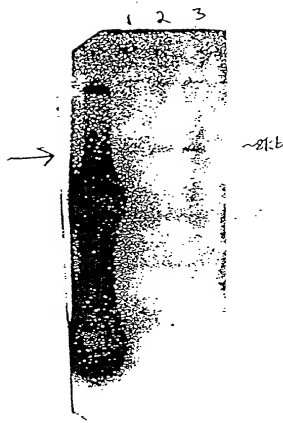


FIG. 30

09470820-106504

10 20 30 40 50
 RCHDS28.COMPLETE.SEQ (1>128)-> GGGAGGTGGGCTCCTGCTCATCTAGGCATCGCACTGATGTTTACCTGTT
 GGGAGGTGGGCTCCTGCTCATCTAGGCATCGCACTGATGTTTACCTGTT

60 70 80 90 100
 RCHDS28.COMPLETE.SEQ (1>128)-> GCAGAAAGAATAAAAAATGACATAAGCAAACCTCATCTTCAAAAGTGGAGAT
 GCAGAAAGAATAAAAAATGACATAAGCAAACCTCATCTTCAAAAGTGGAGAT

110 120
 RCHDS28.COMPLETE.SEQ (1>128)-> TTCCAAATGTCCCGTATGCTGAATAAC
 TTCCAAATGTCCCGTATGCTGAATAAC

FIG. 31

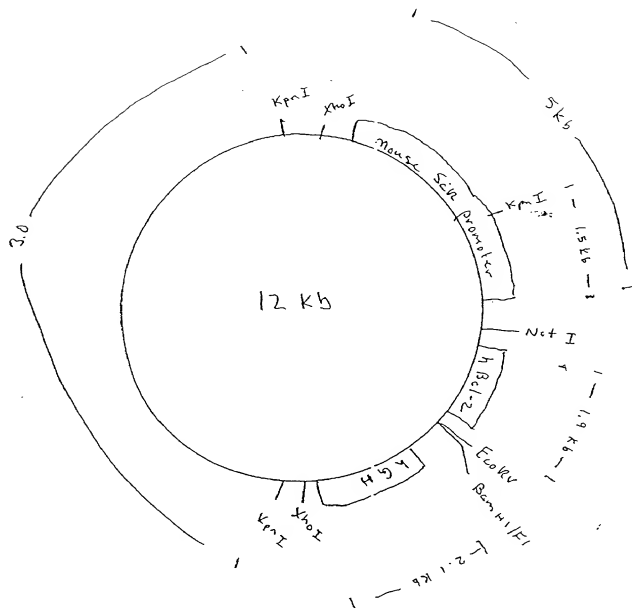


FIG. 32

09970820-100504

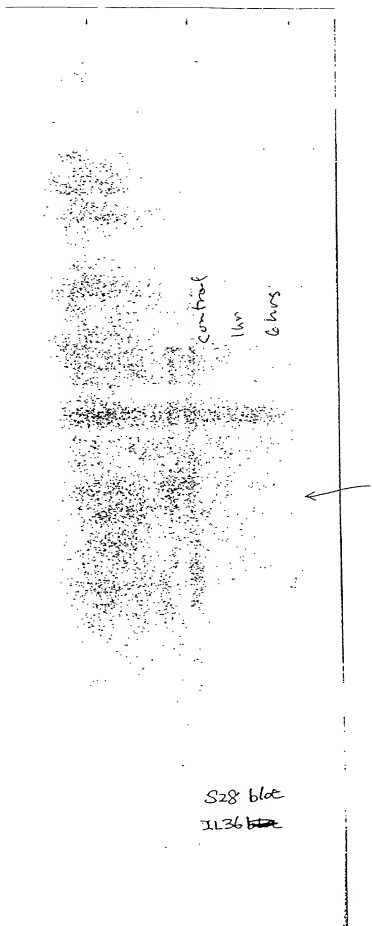


FIG. 33

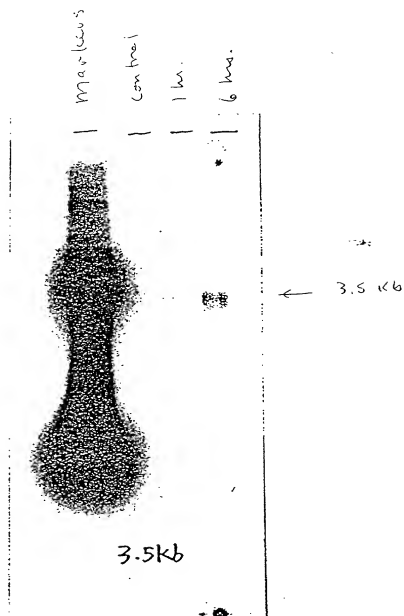


FIG. 34

PCID534

GAATTGGGACGAGGCGAGGAGCTCCTTTCAGCTGCGCTCCCATCATGGGGCTTAGGGTTGAGTCTTCA 68

GCTTCTGGGGGAGGAGGACGGGCACTGAGAGGCCCCCTCCCATCATCAGAGCCCTCTTTGGAGGGGGGAACTTG 147

GCACCCCCGGGACATGTGGATCTTTCTTANGCAGATCTCAGCTGGAGAGATGGGGGTGTAAAGTTAAATGCCCAA 226

CTGAACCTTTTCCAGGCACTGGGAGAGGCTGTGACTCTTTCTTGGCTTTTGAATTTAGTCTAGATCCCAAAAGGCTA 305

AGTACCCCTGGGGGCTACCCAGAGGACATGCTGGGCTGAGCTGAACCTTCTGTGTACATGGGCCCTGGCTGACTGTCT 384

TTCCTCAGAGAGTTGGAGGAGATTCTGAAAGTTGATTCTCAGGCTGGATGTCCAGGGGGTTGGAGTTTCTGATGTCT 463

TTCCTGCTCCCTCTCTTTCTTCTCTCCCTACAGGCTGACTTCTTTGAGGGGGCTTGGGTCTCAAAAGTCTCT 542

CTGTAAAGTTTAGAGCAAAATGGTTATTAATTTTAAATCAATAAACTTTTAAAGTACTAGACAACCTCTTAAGAGG 621

GGAGTGGAGAGAGGGGCTGTGTGGAGCTCAGGTTCTTTCTGACCTTTGGTGTCTACCCCAAGTGTCCCGCTGAG 700

TGCCCACTTGGCCACCTGAGTAATGGCTTGGGCTCCACAGTCCAGATCCAGAGGGGCGAGCATGTGGGAGTGGC 779

GGCTGATGTTTACCCAGTATGTTTGAAGGCAATTATCTATACAGGCAAGGAGGAGGCAACCCAAATGTCCATGAG 858

CTGATAAATGGATAAATGAATATGGTAAGTCCAGGATGGATATCATTCACCATGAAAGAGAGAGGATCCGACA 937

CCAAAGGCTGTACACATGGATGAACTTGGATGACTTTCTGCCACATGAAGAGAGAGGCCACCAAAAGGCCATAT 1016

H S R M G K P I E T Q K S P P P 16

ATTGTATGAATGAA ATG TOC AGA ATG GGC AAA CCC ATA GAG ACA CAA AAA TCT CCC CGA CCT 1079

P Y S R L S P R D E Y K P L D L S D S T 36

CCC TAC TCT CCG CTG TCT OCT CCG GAC GAG TAC ANG CCA CTG GAT CTG TOC GAT TOC ACA 1139

L S Y T E T E A T N S L I T A P G E F S 56

TTG TCT TAC ACT GAA AGG GAG GCT ACC AAC TCC CTC ATC ACT GCT CCG GGT GAA TTC TCA 1199

D A S M S P D A T K P S H W C S V A Y W 76

GAC GGC AGC ATG TCT CCG GAC GGC AGC ANG CCG AGC CAC TGG TOC AGC GTG GCG TAC TGG 1259

E H R T R V G R L Y A V Y D Q A V S I F 96

GAG CAC CCG AGG CCG GTG GGC CCG CTC TAT GCG GTG TAC GAC CAG GGC GTC AGC ATC TTC 1319

Y D L P Q G S G F C L G Q L N L E Q R S 116

TAC GAC CTA OCT CAG GGC AGC GGC TTC TGC CTG GGC CAG CTC AAC CTG CAG CAG CCG AGC 1379

E S V R R T R S K I G F G I L L S K E P 136

GAG TCG CTG CCG CGA AGG CCG AGC ANG ATC GGC TTC GGC ATC CTG CTC AGC ANG GAG CCG 1439

D G V W A Y N R G E H P I F V N S P T L 156

GAC GGC GTG TGG GGC TAC AAC CCG GGC GAG CAC CCG ATC TTC GTC AAC TCC CCG AGG CTG 1499

D A P G G R A L V V R K V P P G Y S I K 176

GAC GGC CCG GGC GGC CCG CCG CTG GTG CCG CCG ANG GTG CCG CCC GGC TAC TCC ATC ANG 1559

V F D F E R S G L Q H A P E P D A A D G 196

GAG TTC GAC TTC GAG CCG TCG GGC CTG CAG CAC GGC CCG GAG CCG GAC CCG GGC CAG GGC 1619

P Y D P N S V R I S F A K G W G P C Y S 216

CCC TAC GAC CCG AAC AGC GTC CCG ATC AGC TTC CCG ANG GGC TGG GCG CCG TGC TAC TOC 1679

R Q F I T S C P C W L E I L L N N P R 235

CGG CAG TTC ATC AGC TOC TGC CCG TGC TGG CTG GAG ATC CTC CTC AAC AAC CCG AGA TAG 1739

FIG. 35A

00970820-100001-02802660

TGGGCGCCCGCGGGGCGGGTGGGAGCCCGGCCACCGCACCTGCCGCGCTGGAGAGGGCGGATGCCGAGA 1818
 GACACAGCCCCCAGGACAGAAACCCCCAGATATCATCTACCTAGATTTAATATAAAGTTTATATATATATATGGAAT 1897
 ATATATTATACTTGTAAATATGGAGTCATTTTACAAATGAATATTATATGATGGTGAATGTGTATATGACAA 1976
 ACAGAAAGCGCACTTTGGCTTAATTCCTTCAATACAGATATATTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 2055
 TTTTATATATATATATAAGAAATGATACAGCAGAGCTAGCTGGAAAAGCCTGGGTTTGGTGTATGGTTTTTGAGATA 2134
 TTAATGCCAGACAGAAAAGCTAATACCACTCACTGGATATAAAGTATTGGCATTATAGTTTTTTTAAACTGTCTCT 2213
 TTTTACAAAGAGGGCGAGTAGGGCTTCAGCGGATTTCTGACCATCATGTACCTTGAAACTTGACCTCAGTTTTCAAG 2292
 TTTTACTTTTATTGGATAAAGACAGAACAAATTGAAAAGGAGGAAAGTCACATTTACTCTTAAGTAAACAGAGAAAG 2371
 TTCCTGTGTTCTCTCTCTGCCCAGCTATGGGGTGTCCAGTGGATAGGGATGGCGGTGGGGAAAAGGAGAAATACACTGG 2450
 CCATTTATCTCTGGCAGCTCTTCCAGTCTGATGGAGGAGTTTCATGCCCTAGCCTAGAAAGGCCAGGTCATAGCCC 2529
 CCATCTTTGAGTTATGAGCAAGCTAAAGAGAGCACTATTCTCAACCATTTTGTGGAAATGGCTGGGGAAAGAAAGCT 2608
 GAAATGGGCTTGAGGCCACCTGCTACCTTCAGAGAACCATCTGAGCGCCCTAGATCTTTTTTAGGACCTCCACAGGC 2687
 TATTTCCACCCCCCGACCAAAATAGCTGAGATCTGCCCATCGAGGGCTGATTAATGATTTATGTAAGGCGAGTG 2766
 GTTATTCTACTTTGTAAAGGAGAAAGTTGAGGTTCTGGAGGATAAATGATTGTCTCATGAGACAAAATCAGGTT 2845
 AGAGTTCATGGAATTGTAGGACGAGGACATATCATTTAGATCAGCTTTCTGAAGAATATTCTCAAAAAAGAAATC 2924
 TCCCTGGCCAGATAACTAAGAGGAATGTTTCATGTATATCTTTTCTCTGGAGATTATATTAACATATTAAGTGCTC 3003
 TGAGAGTGCTCTGTATTATCTCTGCTGCATAAATATATCCCAAACTTAAAAAAGAAAAAAGAAATACGAA 3082
 G 3083

FIG. 35B